

CDC7 Gene Structure

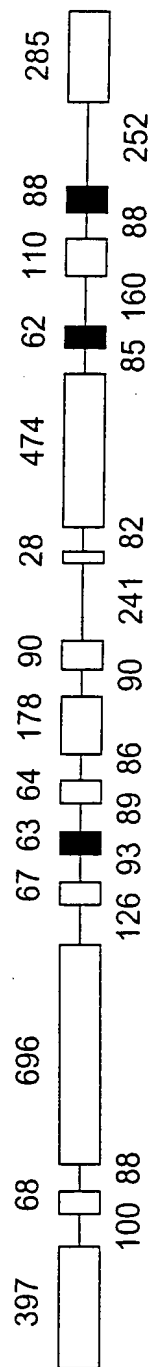


FIGURE 1

CDC27A1 Gene Structure

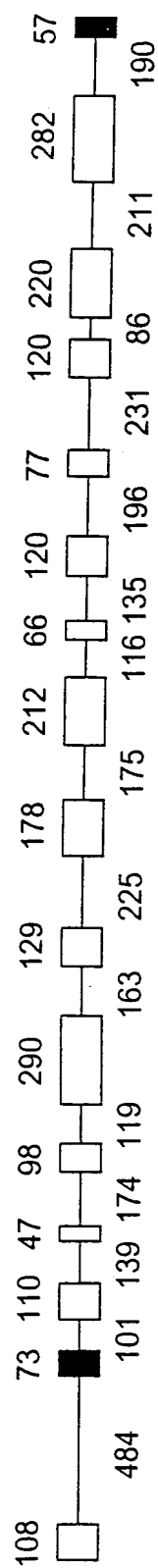


FIGURE 2

[illegible]

1' ATGTCAGAAAACTCGGAACCGCGTCAACTCGAGAATTCTACA 60
TCTAAGTGTCTGTAACGTTACAGTCTTTTTGAGCCTTGGCGCAGTTGAGCTCTTAAGATGT
M S E N S E P R Q L E N S T -
61 GCCGGAAGAGAGCTCATTCTCTAGTCCCACCAATTCAGACGGCAACGACGACCTTAAC 120
CGGCCTTCTCTCGAGTAAGGAGAATCAGGGTGGTTAAGTCTGCCCTTGGCTGCTGGAATTG
A G R E L I P L S P T N S D G N D D L N -
121 TATCATCTGCAATGCTTTTGAGTTATCTCGTCTCCTACTTTCTTCTGGTCAATCCAGAATCT 180
ATAGTAGACGTACGAAAACTCAATAGAGCAGAGGATGAAAGAAGACCAGTAGGTCTTAGA
Y H L H A F E L S R L L L S S G H P E S -
181 GTTATAGATCTTTCTTCAAAGTGTACATACTTCCAAGGTTCTCCTAATCTCGTCAAATAT 240
CAATATCTAGAAAGAAGTTTTCATGTATGAAGGTTCCAAGAGGATTAGAGCAGTTTATA
V I D L S S K C T V F Q G S P N L V K Y -
241 CTTTGCTCGATCCCTAATTCTCCTATTTCCCTTGGCGAAGATGGCTTCAGTGTGACTCTC 300
GAAACGAGCTAGGGATTAAGAGGATAAAGGGAACGGCTTCTACCGAAGTGACACTGAGAG
L C S I P N S P I S L A E D G F T V T L -
301 TCGCCTGAGTCTCCCTCCGCTCCGGCTAGTTTCGCGCTGTAGTTTGGATTTGCAGGAAAAAT 360
AGCGGACTCAGAGGGAGGCGAGGCCGATCAAAGCGGACATCAAACCTAAACGTCTTTTAA
S P E S P S A P A S F A C S L D L Q E N -
361 GTTGTGTTAGAACAGTTTATGGATCCGAGATCTCTCAGCTAAAGCATTGAGAGAGAAT 420
CAACACAATCTTGTCAAATACCTAGGCTCTAGAGAGTGCAGATTTCGTAAGCTCTCTCTTA
V V L E Q F M D P R S L T L K H S R E N -
421 GCGGAACAAGAGGAGCTAGAGCTCATGCCATTGCCCAAAAGAAGTCGAAATGATGGAAC 480
CGCCTTGTCTCTCGATCTCGAGTACGGTAACGGGTTTTCTTCAGCTTTACTACCTTTG
A E Q E E L E L M P L P K R S R N D G N -

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43
481 GATGTGAATTAATGTAATAGTAGCGACCTAACGACATCGAACTGTGGCCGTGGGA 540
CTACACTTAATGAGACATTAATCTATCGTCTGGATTGCTGTAGTCTTGAACACGACACCT
43
D V N Y S V I D S R E N D I R T V A C G -
541 ACTATGCTTGGGACCTATTTTAGCTCTTGAATCCCAAGCTTCCGTTTTCATTTAAGTGC 500
TGATACGAACCCCTGATAAAATCGAGAACTTAGGGTTCGAAGCCAAAAGTTAAATTACCT
T M L G T I L A L E S Q A S V E N L S A -
601 TCTAACCGAGGAATAGAGGGCTTTTGTTCAGATCATCAGCCTGGTCCGCGAGCATCCAAAT 560
AGATTGGCTCTCTTATCTCCGAAAACAGAGTCTAGTAGTCCGACCGGGCTCTGTAGGTTA
S N R G I E A F V Q D E Q E G P Q T S N -
661 GCTTCAGTGGATGTCAATCCTACACATCGGTTAGAGGAAAGCAAGAACGATTTGCCATCT 720
CGAAGTCACTACAGTTAGATGTGTAGCCCAATCTCTCTTCGTTCTTGGCTAAACGGTGA
A S V D V N P T E R L E E S K N D L P S -
721 CCTCAGGAGGATGGATATTACGAGCGACCTGAAATTGGAGATTTCCAAATTGCTGACAAC 780
GGAGTCTCTCTACCTATAATGCTCGCTGCACTTTAAACCTCTAAAGGTTTAAACGACTGTG
P Q E D G Y Y E R P E I G D F Q I A D N -
781 CAAATATTAATCGAAGAAGGTGATGATAAAAAATAAGAAGGATCTCTTCCCTAAGGGAGAG 840
GTTTATAATTAGCTTCTTCCACTACTATTTTATCTCTCTAGAGGAAGGGATTCCCTCTC
Q I L I E E G D D K N K K D L F P K G E -
841 ATACAAACTGATTCTGTGTCAGTCCGATCCCGTTGCTTCATTGATGCCAACAGAAAATGAG 900
TATGTTTGACTAAGACACGTGAGGCTAGGGCAACGGAGTAACTACGGTTGTCTTTTACTC
I Q T D S V Q S D P V A S L M P T E N E -
901 TTAGAACCAGTGCAGATTGTGGATGACACTGAAGATCTACTTGTAGATGATCACAATGTA 960
AATCTTGGTCACGTCTAACACCTACTGTGACTTCTAGATGAACATCTACTAGTGTGACAT
L E P V Q I V D D T E D L L V D D H T V -
961 GACATCGTTAGCACCCCTGACAGAGAGCTGCCGTTGAAGCCTTCTGCTACAGAAGCTAAT 1020
CTGTAGCAATCGTGGGGACTGTCTCTCGACGGCAACTTCGGAAGACGATGTCTTCGATTA
D I V S T P D R E L P L K P S A T E A N -
1021 CAGATAAATCTTTGGTACAAAAACTCTGGATCAATGCAAAATGCCGGGAAACAGCAAA 1080
GTTCTATTTAGAAACCATGTTTTTTGAGACCTAGTTACGTTTAAACGGCCCTTTGTCTTT

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Q D K S L V Q K T L D Q C K L E G N S K -
ACGTACAGCTGTTCCCTGAGATAAAACACACCAGAAAAAGTAAAGTTATCCAGAAGAGG 1140
1081 TGCATGTCGACAGGGGACTCTATTTTGTGTGGTCTTTTTCATTTCATAGGTCCTCTCC
T Y S C S P E I K E T R K S K V I Q K R -
AAGCGAATTTTAAACACCGTTCGTCTTAAAGATCAGAAGGATCAGGCAAGCATAACCA 1200
1141 TTCGTCTTAAATTTGTGGCAAGCAGAAATTTCTAGTCTTCTCCTAGTCCGTTTCGTATTGTGT
K Q N F N T V R L K D Q K D Q A K E N T -
ATTCCAGATTTTGATTCTTACACTATTGTAGAGGAAGAAGGTTCAAGTGGCTACGGGATT 1260
1201 TAAGGTCTAAAACTAAGAATGTGATAACATCTCTCTCTCCAAGTCCACCGATGCCCTAA
I P D F D S Y T I V E E E G S G G Y G I -
GTTTATAAGGCACCGAGGAAAACCTGATGGAACAGAGTTTGCAATTAATGCCCTCATGTT 1320
1261 CAAATATTCCGTTGCTCTCTTTGACTACCTTGTCTCAAACGTTAATTTACGGGAGTACAA
V Y K A T R K T D G T E F A I K C B H V -
GGCGCTCAGAAGTATTATGTGAATAATGAAATCAGAATGCTCGAGCGTTTTGGGGGAAA 1380
1321 CCGCGAGTCTTCATAATACACTTATTACTTTAGTCTTACGACCTCGCAAAACCCCCCTTT
G A Q K Y Y V N N E I R M L E R F G G K -
AACTGTATAATAAAGCATGAAGGCTGTCTCAAGAATGGAGATTCTGATTGCATCATCCTT 1440
1381 TTGACATATTATTTTCGTACTTCCGACAGAGTTCTTACCTCTAAGACTAACGTAGTAGGAA
N C I I K H E G C L K N G D S D C I I L -
GAGCACCTTGAACATGACAGACCTGATTCTTGAAGAGAGAAATAGATGTGTATCAGCTG 1500
1441 CTCGTGGAACCTTGTACTGTCTGGACTAAGTAACTTCTCTCTTTATCTACACATAGTCGAC
E H L E H D R P D S L K R E I D V Y Q L -
CAGTGGTACGGCTACTGCATGTTCAAAGCTCTATCGAGTCTGCATAAGCAGGTTGTGTT 1560
1501 GTCACCATGCCGATGACGTACAAGTTTCGAGATAGCTCAGACGTATTCTGTCCTCCACAACAA
Q W Y G Y C M F K A L S S L H K Q G V V -
CATAGGGATGTTAAGCCAGGAACTTCCTCTCTCTAGGAAGACCAACAAAGGCTATCTC 1620
1561 GTATCCCTACAATTCGGTCTCTTTGAAGGAGAAGAGATCCTTCTGGTTGTTTCCGATAGAG
H R D V K P G N F L F S R K T N K G Y L -
ATTGATTTTAACTTGCCATGATTGTCACCAAGTACAGAAGAGCAGATAAATCAAAA

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1621 ----- 1680
TAACTAAAATTGGAACGGTACCTAAACGGTGGTCTTCATGTCTTCCTGTCCTATTTAGTTTT
8/9 9/10
I D E N L A M D L H Q K Y R R A D K S K -
GCGAGCTTCAGGTCTTCCTACCGCCAGCAAGAAACATCATACTTGGTTAAATCACTCCGAT
1681 ----- 1740
CGTCCGAAGTCCAGAAGGATGGCGGTCTCTTGTAGTATGTAACCAATTTAGTGAGCTA
A A S G L P T A S K K H H T L V K S L D -
GCGGTAAACCGAGGGACCAACAAACCTTCTCAGAAAACCTTTAGCCCTTAATAGTATCAAG
1741 ----- 1800
CGCCATTGGGTCTCCCTGGTTGTGTTGGAAGAGTCTTTTGAAATCGCGGATTATCATAGTTC
A V N R G T N K P S Q K T L A P N S I K -
AAAGCAGCGGGAAAGACAAGAGCTCGGAATGCATGACCAGATGGGAGAGACTCAATAGC
1801 ----- 1860
TTTCGTGCGCCCTTTCTGTCTCTGAGCCCTTACTGTACTGGTCTACCCCTCTCTGAGTTATCG
K A A G K T R A R N D M T R W E R L N S -
CAGGGGCGAGAAGGGTCTGGCTTAACTTCAGCTAAAGATGTGACCAGCAAGGAACAAC
1861 ----- 1920
GTTCCCCGTCTTCTCCAGACCGAATTGAAGTCGATTCTACACTGGTCTGTCTCTCTGTTG
Q G A E G S G L T S A K D V T S T R N N -
CCTTCAGGTGAAAAGAGAAGAGAGCCTTTGCCATGTCTATGGAAGAAAAGCGCTTTTATAGAT
1921 ----- 1980
GGAAGTCCACTTTTCTCTCTCTCGGAAACGGTACAGTACCTTCTTTTCCGGAATCTA
P S G E K R R E P L P C H G R K A L L D -
TTTCTGCAAGAGACAATGTCTGTCTCCAATTCCAAACCATGAAGTATCATCCAAAGCTCCT
1981 ----- 2040
AAAGACGTTCTCTGTTACAGACAAGGTTAAGGTTTGGTACTTCATAGTAGGTTTCGAGGA
F L Q E T M S V P I P N H E V S S K A P -
ACGTCTATGAGAAAACGGGTAGCTGCTCTTCCAGGGAAAGCTGAGAAGGAACTTCTTTAT
2041 ----- 2100
TGCAGATACTCTTTTGCCCATCGACGAGAAGGTCCCTTTCGACTCTTCTCTGAAGAAATA
T S M R K R V A A L P G K A E K E L L Y -
CTGACCCCAATGCCACTGTGCTCTAACGGTCTGGCCCTGAAGCAGGGGACGTAATTGAGAAG
2101 ----- 2160
GACTGGGGTTACGGTGACACGAGATTGCCAGCCGACTTCGTCCCTGCATTAACTCTTC
10/11
L T P M P L C S N G R P E A G D V I E K -
11/12
AAAGACGGTCTCTGCTCAGGAACCAAGGCTTCCGAGCTCCAGAGGTTTGTCTCAGATCT
2161 ----- 2220
TTTCTGCCAGGAACGAGTCTTTGGTTTCCGAAGGCTCGAGGTCTCCAAACGAAGTCTAGA
11/12
K D G P C S G T K G F R A P E V C F R S -

2221 TTGCACTAAGGACCTAAGATAGACGTGTGGTCTGCGGGAGTTA¹²CTTTGTATACCTCATA 2280
AACGTGGTTTCCTGGATTCTCTGCAACCGACGCCCTCAATGAAACATATGGAGTAT
L H Q G E K I D V W S A G V T L L Y L I -
2281 ATGGGAAGGACACCTTTCACTGGTGACCTGAAAC¹²GAACATAAAGGACATTGGCACTA 2340
TACCTTCTCTGTGGAAAGTGACCACTGGGACTTGTCTTGTATTTCTGTAACTGTGTGAT
M G R T P F T G D E E Q¹²N I K D I A Q L -
2341 CGAGGCAGTGAAGAATTATGGGAAGTAGCCAAGCTGCACAACCGTGAATCCTCTTTCCCT 2400
GCTCCGTCACCTCTTAATACCTTTCATCGGTTTCGACGTGTGTGGCACTTAGCAGAAAGGGA
R G S E E L W E V A K L E N R E S S F P -
2401 AAGGAATTATACGAGTCAAGGTACTTGAAGGGGATGGAGTTGAGAAAATGGTGCGAACTC 2460
TTCTTAATATGCTCAGTTCCATGAACCTTCCCTACCTCAACTCTTTTACCACGCTTGAG
K¹³E L Y E S R Y L K G M E L R K W C E L -
2461 AACACAAAACGCAGAGAGTTTCTAGACGTAATTCCTACTATCGCTTCTTGACCTCGTTGAT 2520
TTGTGTTTTGCGTCTCTCAAAGATCTGCATTAAAGGTGATAGCGAAGAACTGGAGCACTA
N T K R R E F L D V I P L S L L D L V D -
2521 AAATGTTTTGACCGTTAACCCGAGGCGACGAATCAGCGCAGAGGATGCTCTCAAGCACGAC 2580
TTTACAAACTGGCAATTGGGCTCCGCTGCTTAGTCCGCTCTCCTACGAGAGTTTCGTGCTG
K C L T V N P R R R I S A E D A L K H D -
2581 TTCTTCCATCCAGTACATGAAACCTTAGAAACCAATGCTCCTTAAACAGCAGCCTACA 2640
AAGAAGGTAGGTCATGTACTTTGGCAATCTTTGGTTTACGAGGAATTTGTCTGTCGGATGT
F F H P V H E T L R N Q M L L K Q Q P T -
2641 GTGGTTGCTGACGCGAGTAAGCCAACTCTAAACTATTTACAATTGTAAAGTAAATAAG 2699
CACCAACGACTGCGTCATTCCGTTTGGAGTTTGATAAATGTTAACATTTTCAATTTATTC
V V A D A V S Q T L N Y L Q L *

[illegible]

1
CCGCTGTAATGTGTGTGTCGGAGGCTCCCTGTGTGTGTGTGTAGCTAACGAGCCAGTTAAA
60

61
ATGATGGAGAATCTACTGGCGAATTGTGTGCCAGAAAAACCTT
120
CCAGTAGTAGTAGTAGTCTACTACCTCTTAGATGACCGCTTAACACAGGTCTTTTTCGGAA

121
M M E N L L A N C V Q K N L
180
AACCATTTTATGTTCCACCAATGCTATCTTCCTTTGGCGAAGTTCTTCTCGCCCAATTTCCA
TTGGTAAAAATACAGTGGTTACGATAGAAGGAAACGCTTGAAGAAGACGGGGTTAAAGGT

N H F M F T N A I F L C E L L L A Q F P
181
TCTGAGGTGAACCTGCAATTGTTAGCCAGGTGTTACTTGGAGTAACAGTCAAGCTTATAGT
240
AGACTCCACTTGGACGTTAAACAATCGGTCCACAATGAAGTCAATTGTCAGTTCGAATATCA

S E V N L Q L L A R C Y L S N S Q A Y S
241
GCATATTATATCCTTAAAGGTTCAAAAACGCCTCAGTCTCGGTATTTATTTGCAATTCTCA
300
CGTATAATATAGGAATTTCCAAAGTTTTTGGCGAGTCAGAGCCATAAATAAACGTAAGAGT

A Y Y I L K G S K T P Q S R Y L F A F S
301
TGCTTTAAGTTGGATCTTCTTGGAGAGGCTGAAGCTGCATTGTTGCCCTGTGAAGATTAT
360
ACGAAATTCAACCTAGAAGAAGCTCTCCGACTTCGACGTAACAACGGGACACTTCTAATA

C F K L D L L G E A E A A L L P C E D Y
361
GCTGAAGAAGTTCCCTGGTGGTGCAGCTGGGCATTATCTTCTTGGTCTTATATATAGATAT
420
CGACTTCTTCAAGGACCACCACGTCGACCCGTAATAGAGAACCAGAATATATATCTATA

A E E V P G G A A G H Y L L G L I Y R Y

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7|8
901 AACTTTTTTAGTGAAGAATTGTGAGCAGAGGCTCAAGAAGAATCTGGGCGCCGCCSTAGT 960
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TTGAAAAAATCACTTCTTAACAGTTCGTCTCCGAGTTCTTCTTAGACCCGCGGCGGCATCA
7|8
N F F S E E L S A E A Q E E S G R R R S
GCTAGAATAGCAGCAAGGAAAAAGAATCCTATGTGCGCAGTCATTTGGAAAAGATTCCCAT
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
CGATCTTATCGTTCGTTCTTCTTTTCTTAGGATACAGCGTCAGTAAACCTTTTCTAAGGGTA
A R I A A R K K N P M S Q S F G K D S H
TGGTTACATCTTTTACCTTCCGAGTCAAACCTATGCACCTTCTCTTTCCCTCGATGATTGGA
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
ACCAATGTAGAAAGTGGAAGGCTCAGTTTGATACGTGGAAGAGAAAGCAGCTACTAACCT
W L H L S P S E S N Y A P S L S S M I G
8|9
AAATGCAGAATCCAAAGCAGCAAAGAAGCGATTCCGTGATACCGTTACTCTAAATGATCCA
1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
TTTACGTCTTAGGTTTCGTTCGTTTCTTCGTAAGGACTAIGGCAATGAGATTTACTAGGT
8|9
K C R I Q S S K E A I P D T V T L N D P
GCAACGACGTCAGGCCAGTCTGTAAAGTGACACTGGAAGCTCTGTTGATGATGAGGAAAAG
1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
CGTTGCTGCGAGTCCGGTCAGACATTCAGTGTGACCTTCGAGACAATACTACTCTCTTTTC
A T T S G Q S V S D T G S S V D D E E K
TCAAATCCTAGTGAATCTTCCCCGATCGTTTCAGCCTTATTTCTGGAATTTCAGAAGTG
1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
AGTTTAGGATCACTTAGAAGGGGCCTAGCAAAGTCGGAATAAAGACCTTAAAGTCTTCAC
S N P S E S S P D R F S L I S G I S E V
9|
CTAGGCATTCTGAAAATCTTGGAGATGGCCACAGGCATTTACATATGTACAAGTGTGAG
1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320
GATCCGTAAGACTTTTAAAGAACCTCTACCGGTGTCCGTAAATGTATACATGTTTACAGTC
9|
L G I L K I L G D G H R H L H M Y K C Q

¹⁰
 1321 GAAGCTTTGTTGGCATATCAAAAGCTATCTCAGAAACAATAACAATAACAACCTGGGTTCTC 1380
 CTTCTGAAACAACCGTATAGTTTTTCGATAGAGTCTTTGTTATGTTATGTGTGACCCAAGAG
¹⁰
 E A L L A Y Q K L S Q K Q Y N T H W V L
¹⁰¹¹
 1381 ATGCAGGTTGGAAAAGCATATTTTGAGCTACAAGACTACTTCAACGCTGACTCTTCCTTT 1440
 TACGTCCAACCTTTTCGTATAAAACTCGATGTTCTGATGAAGTTGCGACTGAGAAGGAAA
¹⁰¹¹
 M Q V G K A Y E E L Q D Y F N A D S S F
 ACTCTTGCTCATCAAAAGTATCCTTATGCTTTGGAAGGAATGGATACATACTCCACTGTT
 1441 TGAGAACGAGTAGTTTTTCATAGGAATACGAAACCTTCCTTACCTATGTATGAGGTGACAA 1500
 T L A H Q K Y P Y A L E G M D T Y S T V
¹¹¹²
 1501 CTTTATCACCTGAAAGAAGAGATGAGGTTGGGCTATCTGGCTCAGGAACTGATTTTCAGTT 1560
 GAAATAGTGGACTTTCTTCTCTACTCCAACCCGATAGACCGAGTCCTTGACTAAAGTCAA
¹¹¹²
 L Y H L K E E M R L G Y L A Q E L I S V
¹²¹³
 1561 GATCGCCTGTCTCCAGAATCCTGTTGTGTCAGTTGGGAACCTGTTACAGTTTGCCTAAGGAT 1620
 CTAGCGGACAGAGGTCTTAGGACCACACGTCAACCCTTGACAATGTCAAACGCATTCTCTA
¹²¹³
 D R L S P E S W C A V G N C Y S L R K D
 CATGATACTGCTCTCAAAATGTTTTCAGAGAGCTATCCAACCTGAATGAAAGATTCACATAT
 1621 GTACTATGACGAGAGTTTTTACAAAGTCTCTCGATAGGTTGACTTACTTTCTAAGTGTATA 1680
 H D T A L K M F Q R A I Q L N E R F T Y
¹³¹⁴
 1681 GCACATACCTTTTGTGGCCACGAGTTTGGCCGATTGGAAGAATTCGAGGATGCAGAGAGA 1740
 CGTGTATGGGAAACACCGGTGCTCAAACGGCGTAACCTTCTTAAGCTCCTACGTCTCTCT
¹³¹⁴
 A H T L C G H E F A A L E E F E D A E R
 TGCTACCGGAAGGCTCTGGGCATAGATACGAGACACTATAATGCATGGTACGGTCTTGGA
 1741 ACGATGGCCTTCCGAGACCCGTATCTATGCTCTGTGATATTACGTACCATGCCAGAACCT 1800
 C Y R K A L G I D T R H Y N A W Y G L G -

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ATGACCTATCTTCGTCAGGAGAAATTCGAGTTTGCGCAGCATCAATTTCAACTGGCTCTC
1801 -----+-----+-----+-----+-----+ 1860
TACTGGATAGAAGCAGTCCTCTTTAAGCTCAAACGCGTCGTAGTTAAAGTTGACCGAGAG

M T Y L R Q E K F E F A Q H Q F Q L A L

CAAATAAATCCAAGATCTTCAGTCATCATGTGTTACTATGGAATTGCTTTGCATGAGTCA
1861 -----+-----+-----+-----+-----+ 1920
GTTTATTTAGGTTCTAGAAGTCAGTAGTACACAATGATACCTTAACGAAACGTACTCAGT

Q I N P R S S V I M C Y Y G I A L H E S
14/15
AAGAGAAACGATGAGGCGTTGATGATGATGGAGAAGGCTGTACTCACTGATGCAAAGAAT
1921 -----+-----+-----+-----+-----+ 1980
TTCTCTTTGCTACTCCGCAACTACTACTACCTCTTCCGACATGAGTGACTACGTTTCTTA
14/15
K R N D E A L M M M E K A V L T D A K N

CCGCTCCCCAAGTACTACAAGGCTCACATATTAACCAGCCTAGGTGATTATCACAAGCA
1981 -----+-----+-----+-----+-----+ 2040
GGCGAGGGGTTTCATGATGTTCCGAGTGTATAATTGGTCCGATCCACTAATAGTGTTCGTT

P L P K Y Y K A H I L T S L G D Y H K A

CAGAAAGTTTLAGAAGAGCTCAAAGAATGTGCTCCTCAAGAAAGCAGTGTCCATGCCATCG
2041 -----+-----+-----+-----+-----+ 2100
GTCTTTCAAAATCTTCTCGAGTTTCTTACACGAGGAGTTCTTTCGTCACAGGTACGTAGC

Q K V L E E L K E C A P Q E S S V H A S

CTTGGCAAAATATACAATCAGCTAAAGCAATACGACAAAGCCGTGTTACATTTGGGCATT
2101 -----+-----+-----+-----+-----+ 2160
GAACCGTTTTATATGTTAGTCGATTTTCGTTATGCTGTTTCGGCACAATGTAAAGCCGTAA

L G K I Y N Q L K Q Y D K A V L H F G I
15,16
GCTTTGGATTTAAGCCCTTCTCCATCTGATGCTGTCAAGATAAAGGCTTACATGGAGAGG
2161 -----+-----+-----+-----+-----+ 2220
CGAAACCTAAATTCGGGAAGAGGTAGACTACGACAGTTCTATTTCCGAATGTACCTCTCC
15,16
A L D L S P S P S D A V K I K A Y M E R

2221 TGGATACTACCGAGCGAGCTGGTGACGGAGGAAAATTTGTAGATTATTTGTGCGGTAAT 2280
 AACTATGATGGTCTGCTCGACCACTGGCTCCTTTTAAACATCTAAATAACACGTCCTTA
 L I L P D E L V T E E N L *
 2281 ACACCGATTATGTTTCTCATATAACCCAAAGTCATCTGTAATTTTCTCATCTTTAGAT 2340
 TGTGGTCTAATACAAAGAGTATATTGGGTTTCAGTAGACATTAAAAAGAGTAGAAATCTA

 2341 CAGTCTTGTGGACTAACCCTAAAACAAAACCTGATTATATAAACTTAGAGGTAATATTAC 2400
 GTCAGAACACCTGATTGGGATTTTGTCTTACTAATATATTTGAATCTCCATTATAATG

 2401 AGAAAATGTTATAGAGTTGGGTTTGAATTTTCTTTTCTTTTCCAAGTTGGAACTTTTGT 2460
 TCTTTTAACATATCTCAACCCAAACTTAAAAGTAAAGAAAAGGTTCAACCTTGAAAACAA

 2461 CAAA 2512
 GTT

2461 ----- 2512

CDC27B Gene Structure

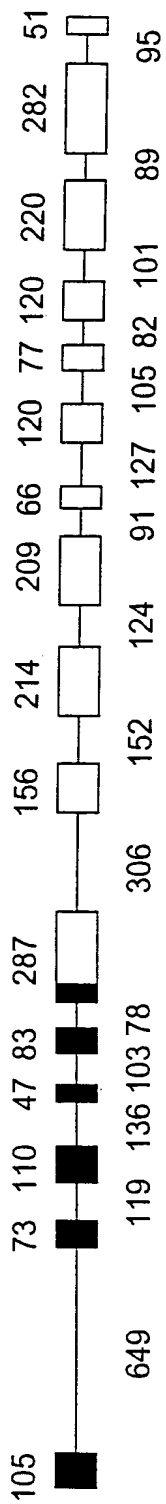


FIGURE 5

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SEQ ID NO 6
Cdc27A1 1- MMENLLANCVQKNLNHFMTNAIFLCELLLAQFPSEVNLQOLLARCYLSNS
Cdc27B 1- MEAMLV-DCVNNSLRHFVYKNAIFMCERLCAEFPSEVNLQOLLATSYLONN

SEQ ID NO 10
SEQ ID NO 6
Cdc27A1 51- QAYSAYYILKGSKTPQSRYLFAFSCFKLDLLGEAEAALLP-CEDYABEVP
Cdc27B 50- QAYSAYHLLKGTQMAQSRYLFAFSCFQMDLLNEAESALCPVNEPGAE-IP

SEQ ID NO 10
Cdc27A1 100- GGAAGHYLLGLIYRYSGRKNCISQOFRMALSFDPWCWEAYGELCSLGAAE
Cdc27B 99- NGAAGHYLLGLIY----KKNAA-QQFKQSLTIDPLLWAAAYEELCILGAAE

SEQ ID NO 10
Cdc27A1 150- EASTVFCNVASQRIQKTCVEQRISFSEG-ATIDQ--ITDSDKAL--KDTG
Cdc27B 144- EATAVFGETAALSTQKQYMQQ-LSTSLGLNTYNEERNSTSTKNTSSSEDYS

SEQ ID NO 10
Cdc27A1 194- LSQTEHIPGENQODLKIMQOPGDIPPNTDRQLSTNGWDLNTPSPVLLQVM
Cdc27B 193- PROSKHTQSHGLKDISGNFHSBGVNGGV----SNMSFY-NTPSPVAAQLS

Cdc27A1 244- D-APPPELL NMRRPAV-EG-SLMS-----VHG-VRVRRRNFSE---
Cdc27B 238- GIAPPPEL-FRNFO-PAVANPNSLITDSSPKSTVNSTLQAPRRKEVDEGKL

Cdc27A1 280- -ELSAEAQEEESG-RRRSARIAA-----RKNPMSSQSFQKDSHWLHLSP
Cdc27B 286- RKISGRLFSDSGPRR-SSRLSADSGANINSSVATVSGNVNNAASKYLGGSK

SEQ ID NO 12
Cdc27A1 321- SESNYAPSLSMMIGKCRIQSSK-----EAIPD-TV-----TLNDPA
Cdc27B 335- -----LSSLALRS-VTLRKGHSWANENM-DEGVGEFPDDSRPNTAS

Cdc27A1 356- TTSGQSVSDTGSSVDDEEKSNPSE--SSPDRFSLIS-GISEVLSTLKILG
Cdc27B 375- TTGSMASND----QEDETMSIGGIAMSSQT----ITIGVSEILNLLRTL

Cdc27A1 403- DGRHRLHMYKCOEALLAYOKLSQKQYNTHWVLMQVQKAYFELQDYFNADS
Cdc27B 417- EGCRLSYMYRCOEALDTYMKLPHKHYNTGWVLSQVQKAYFELIDYLEAEK

Cdc27A1 453- SFTLAHQKYPYALEGMDTYSTVLYHLKEEMRLGYLAQELISVDRLSPESW
Cdc27B 467- AERLARLASPYCLEGMDTYSTVLYHLKEDMKLSYLAQELISTDRLAPQSW

Cdc27A1 503- CAVGNCYSLRKDHDOTALKMFORAIQLNERTYAHTLCGHEFAALEEFEDA
Cdc27B 517- CAMGNCYSLOKDHEOTALKNFLRAVOLNPRFAYHTLCGHEYTTLEDFFENG

Cdc27A1 553- ERCYRKALGIDTRHYNWYGLGMTYLRQEKFEFAQHOFQLALQINPRSSV
Cdc27B 567- MKSYQNALRVDRHYNWYGLGMIYLRQEKLEFSEHFRMAFLINPSSSV

Cdc27A1 603- IMCYYGIALHESKRNDDEALMMMEKAVLTDKNPLPKYKHAHILTSLGDYH
Cdc27B 617- IMSYLGTSLSHALKRSEEALEIMEQATVADRKNPLPMYOKANILVCLERLD

Cdc27A1 653- KAQKVLLEELKECAPOESSVHASL-GKIYNQLKQYDKAVLHFGIALDLSPS
Cdc27B 667- EALEVLEELKEYAPSESSVYA-LMGRIYKRRNMHDKAMLHFGIALDMKPP

SEQ ID NO 7
Cdc27A1 702- PSDAVKIKAYMERLILPDELVTEENL
Cdc27B 716- ATDVAAIKAAMEKLHVPDEIDESP

FIGURE 6

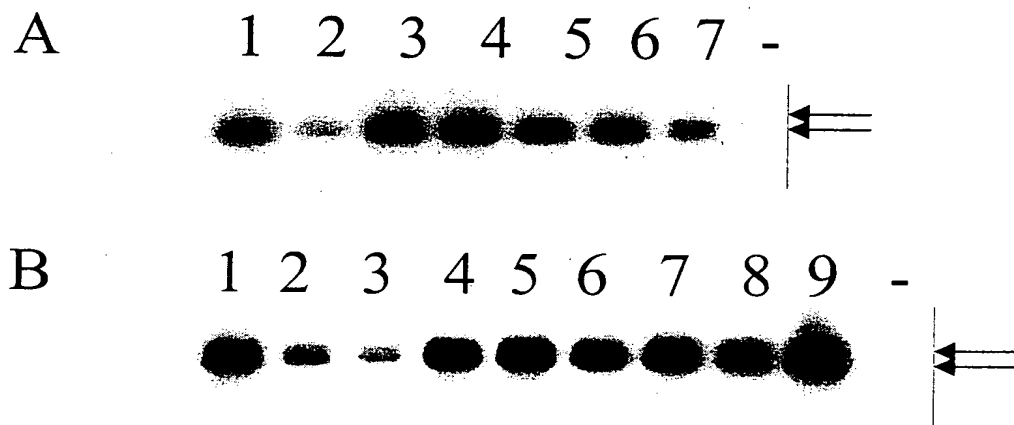


FIGURE 7

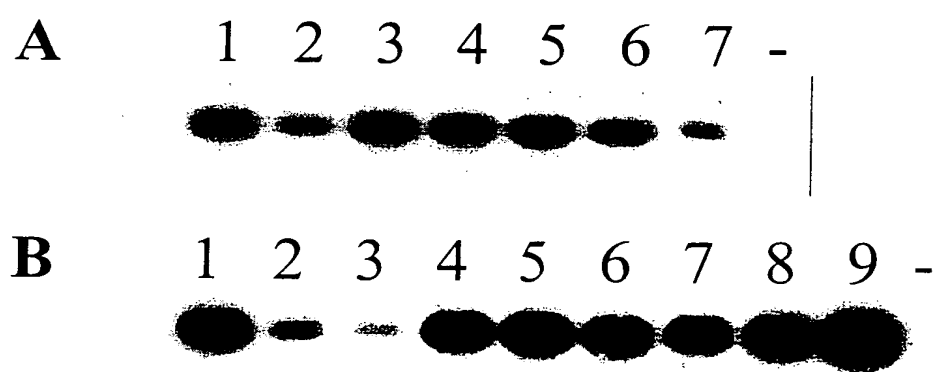


FIGURE 8